

Ne-nun

RAW SEQUENCE LISTING

**The Biotechnology Systems Branch of the Scientific and Technical
Information Center (STIC) no errors detected.**

Application Serial Number: 10/536,935A
Source: JFW
Date Processed by STIC: 6/8/06

ENTERED

NL-NL

RAW SEQUENCE LISTING DATE: 08/08/2006
 PATENT APPLICATION: US/10/536,935A TIME: 18:09:06

Input Set : N:\Crf4\Reffold\10_folder\J536935A.raw
 Output Set: N:\CRF4\08082006\J536935A.raw

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1 <110> APPLICANT: Tsukahara, Kappei
2   Tsuchiya, Mamiko
3   Jigami, Yoshifumi
4   Nakayama, Kenichi
5   Umemura, Mariko
6   Okamoto, Michiyo
7 <120> TITLE OF INVENTION: METHOD OF SCREENING FOR COMPOUNDS THAT
8   INHIBIT THE ENZYMATIC ACTIVITY OF GWT1 GENE PRODUCT
9 <130> FILE REFERENCE: 082368-004400US
C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/536,935A
11 <141> CURRENT FILING DATE: 2005-05-20
12 <150> PRIOR APPLICATION NUMBER: PCT/JP03/14909
13 <151> PRIOR FILING DATE: 2003-11-21
14 <150> PRIOR APPLICATION NUMBER: JP 2002-339418
15 <151> PRIOR FILING DATE: 2002-11-22
16 <160> NUMBER OF SEQ ID NOS: 18
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1497
21 <212> TYPE: DNA
22 <213> ORGANISM: Saccharomyces cerevisiae
23 <220> FEATURE:
24 <221> NAME/KEY: CDS
25 <222> LOCATION: (1)..(1494)
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29     1           5           10          15
30   gag gac ttt gtg aca ggg ctc aat ggc ggt tct ata aca gaa att aac 96
31   Glu Asp Phe Val Thr Gly Leu Asn Gly Ser Ile Thr Glu Ile Asn
32     20          25          30
33   gca gtg aca tca att gct ttg gta act tac ata tca tgg aac tta ttg 144
34   Ala Val Thr Ser Ile Ala Leu Val Thr Tyr Ile Ser Trp Asn Leu Leu
35     35          40          45
36   aaa aat tcc aac ctt atg cct ggc att tcc agc gtg caa tac ata 192
37   Lys Asn Ser Asn Leu Met Pro Pro Gly Ile Ser Ser Val Gln Tyr Ile
38     50          55          60
39   att gat ttt gca ttg aac tgg gtt gct ttg ctt cta tct att act att 240
40   Ile Asp Phe Ala Leu Asn Trp Val Ala Leu Leu Ser Ile Thr Ile
41     65          70          75          80
42   tat gct agt gaa cca tac ctt cta aac acg cta ata ctg tta cct tgt 288
43   Tyr Ala Ser Glu Pro Tyr Leu Leu Asn Thr Leu Ile Leu Leu Pro Cys
44     85          90          95

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45	ttg ctc gca ttc ata tat gga aaa ttt act agc tcg agt aaa cct tct	336
46	Leu Leu Ala Phe Ile Tyr Gly Lys Phe Thr Ser Ser Ser Lys Pro Ser	
47	100 105 110	
48	aat cca ata tac aat aaa aaa atg att aca cag cgg ttc caa cta	384
49	Asn Pro Ile Tyr Asn Lys Lys Met Ile Thr Gln Arg Phe Gln Leu	
50	115 120 125	
51	gaa aaa aag ccg tat att act gcg tat cgt ggt ggg atg ctt att ctg	432
52	Glu Lys Lys Pro Tyr Ile Thr Ala Tyr Arg Gly Gly Met Leu Ile Leu	
53	130 135 140	
54	act gct att gcc atc ttg gct gta gat ttt cca att ttc cca agg agg	480
55	Thr Ala Ile Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro Arg Arg	
56	145 150 155 160	
57	ttt gcc aag gtg gaa act tgg ggg aca tcc ctg atg gat ctt ggt gta	528
58	Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Leu Met Asp Leu Gly Val	
59	165 170 175	
60	gga tca ttc gtt ttc agt aac ggt att gtt tct tct agg gca ctg ttg	576
61	Gly Ser Phe Val Phe Ser Asn Gly Ile Val Ser Ser Arg Ala Leu Leu	
62	180 185 190	
63	aaa aac cta agc ttg aag agt aaa ccc agc ttc tta aaa aat gca ttt	624
64	Lys Asn Leu Ser Leu Lys Ser Lys Pro Ser Phe Leu Lys Asn Ala Phe	
65	195 200 205	
66	aat gcc tta aaa tca gga gga act cta ttg ttc cta gga ttg ctg agg	672
67	Asn Ala Leu Lys Ser Gly Gly Thr Leu Leu Phe Leu Gly Leu Leu Arg	
68	210 215 220	
69	ttg ttt ttt gta aaa aat ttg gaa tat caa gaa cat gtc aca gaa tat	720
70	Leu Phe Phe Val Lys Asn Leu Glu Tyr Gln Glu His Val Thr Glu Tyr	
71	225 230 235 240	
72	ggg gtt cat tgg aat ttt ttg atc acc cta tca ttg ttg cca ctt gta	768
73	Gly Val His Trp Asn Phe Phe Ile Thr Leu Ser Leu Leu Pro Leu Val	
74	245 250 255	
75	ttg acc ttt att gat ccc gtc aca aga atg gtt cca cgc tgc tca att	816
76	Leu Thr Phe Ile Asp Pro Val Thr Arg Met Val Pro Arg Cys Ser Ile	
77	260 265 270	
78	gca ata ttc att tca tgc att tat gaa tgg cta ctt tta aag gac gat	864
79	Ala Ile Phe Ile Ser Cys Ile Tyr Glu Trp Leu Leu Lys Asp Asp	
80	275 280 285	
81	cgc act tta aac ttt tta att ttg gct gat aga aat tgt ttc ttc agt	912
82	Arg Thr Leu Asn Phe Leu Ile Leu Ala Asp Arg Asn Cys Phe Phe Ser	
83	290 295 300	
84	gct aat aga gaa ggc atc ttc tca ttt cta ggt tat tgc tcg att ttt	960
85	Ala Asn Arg Glu Gly Ile Phe Ser Phe Leu Gly Tyr Cys Ser Ile Phe	
86	305 310 315 320	
87	ctt tgg ggc caa aac acg gga ttt tac ttg ttg gga aat aaa cca act	1008
88	Leu Trp Gly Gln Asn Thr Gly Phe Tyr Leu Leu Gly Asn Lys Pro Thr	
89	325 330 335	
90	tta aac aat ctt tat aag cct tct acg caa gac gta gtt gca gca tca	1056
91	Leu Asn Asn Leu Tyr Lys Pro Ser Thr Gln Asp Val Val Ala Ala Ser	
92	340 345 350	
93	aag aag tct tcg act tgg gac tat tgg act tca gta acc cca tta agt	1104

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Input Set : N:\Crf4\Refhold\10_folder\J536935A.raw

Output Set: N:\CRF4\08082006\J536935A.raw

94	Lys Lys Ser Ser Thr Trp Asp Tyr Trp Thr Ser Val Thr Pro Leu Ser			
95	355	360	365	
96	ggc ctc tgt ata tgg agt aca att ttt ctt gtt atc agc cag ttg gtt			1152
97	Gly Leu Cys Ile Trp Ser Thr Ile Phe Leu Val Ile Ser Gln Leu Val			
98	370	375	380	
99	ttt caa tac cat cct tat agt gtt tca aga agg ttt gct aac tta cca			1200
100	Phe Gln Tyr His Pro Tyr Ser Val Ser Arg Arg Phe Ala Asn Leu Pro			
101	385	390	395	400
102	tat act ttg tgg gtc att act tat aat tta cta ttt ttg act ggg tac			1248
103	Tyr Thr Leu Trp Val Ile Thr Tyr Asn Leu Leu Phe Leu Thr Gly Tyr			
104	405	410	415	
105	tgc ttg act gac aaa att ttc ggt aat tct tcg gaa tat tat aaa gtt			1296
106	Cys Leu Thr Asp Lys Ile Phe Gly Asn Ser Ser Glu Tyr Tyr Lys Val			
107	420	425	430	
108	gcc gaa tgc ttg gaa tca atc aac tcc aat ggg ttg ttt tta ttt ttg			1344
109	Ala Glu Cys Leu Glu Ser Ile Asn Ser Asn Gly Leu Phe Leu Phe Leu			
110	435	440	445	
111	ttg gca aat gtc tct act ggt tta gtc aat atg tct atg gtc acg ata			1392
112	Leu Ala Asn Val Ser Thr Gly Leu Val Asn Met Ser Met Val Thr Ile			
113	450	455	460	
114	gat tct tca ccc tta aaa tca ttc ctg gtt ttg ttg gca tac tgc tca			1440
115	Asp Ser Ser Pro Leu Lys Ser Phe Leu Val Leu Leu Ala Tyr Cys Ser			
116	465	470	475	480
117	ttc ata gct gtc ata tcg gtt ttc ttg tat aga aaa aga ata ttc att			1488
118	Phe Ile Ala Val Ile Ser Val Phe Leu Tyr Arg Lys Arg Ile Phe Ile			
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121	Lys Leu			
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124	<211> LENGTH: 498			
125	<212> TYPE: PRT			
126	<213> ORGANISM: Saccharomyces cerevisiae			
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128	Met Ala Thr Val His Gln Lys Asn Met Ser Thr Leu Lys Gln Arg Lys			
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130	Glu Asp Phe Val Thr Gly Leu Asn Gly Gly Ser Ile Thr Glu Ile Asn			
131	20	25	30	
132	Ala Val Thr Ser Ile Ala Leu Val Thr Tyr Ile Ser Trp Asn Leu Leu			
133	35	40	45	
134	Lys Asn Ser Asn Leu Met Pro Pro Gly Ile Ser Ser Val Gln Tyr Ile			
135	50	55	60	
136	Ile Asp Phe Ala Leu Asn Trp Val Ala Leu Leu Leu Ser Ile Thr Ile			
137	65	70	75	80
138	Tyr Ala Ser Glu Pro Tyr Leu Leu Asn Thr Leu Ile Leu Leu Pro Cys			
139	85	90	95	
140	Leu Leu Ala Phe Ile Tyr Gly Lys Phe Thr Ser Ser Ser Lys Pro Ser			
141	100	105	110	
142	Asn Pro Ile Tyr Asn Lys Lys Lys Met Ile Thr Gln Arg Phe Gln Leu			
143	115	120	125	

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TIME: 18:09:06

Input Set : N:\Crf4\Refhold\10_folder\J536935A.raw
 Output Set: N:\CRF4\08082006\J536935A.raw

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144 Glu Lys Lys Pro Tyr Ile Thr Ala Tyr Arg Gly Gly Met Leu Ile Leu
145 130 135 140
146 Thr Ala Ile Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro Arg Arg
147 145 150 155 160
148 Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Leu Met Asp Leu Gly Val
149 165 170 175
150 Gly Ser Phe Val Phe Ser Asn Gly Ile Val Ser Ser Arg Ala Leu Leu
151 180 185 190
152 Lys Asn Leu Ser Leu Lys Ser Lys Pro Ser Phe Leu Lys Asn Ala Phe
153 195 200 205
154 Asn Ala Leu Lys Ser Gly Gly Thr Leu Leu Phe Leu Gly Leu Leu Arg
155 210 215 220
156 Leu Phe Phe Val Lys Asn Leu Glu Tyr Gln Glu His Val Thr Glu Tyr
157 225 230 235 240
158 Gly Val His Trp Asn Phe Phe Ile Thr Leu Ser Leu Leu Pro Leu Val
159 245 250 255
160 Leu Thr Phe Ile Asp Pro Val Thr Arg Met Val Pro Arg Cys Ser Ile
161 260 265 270
162 Ala Ile Phe Ile Ser Cys Ile Tyr Glu Trp Leu Leu Lys Asp Asp
163 275 280 285
164 Arg Thr Leu Asn Phe Leu Ile Leu Ala Asp Arg Asn Cys Phe Phe Ser
165 290 295 300
166 Ala Asn Arg Glu Gly Ile Phe Ser Phe Leu Gly Tyr Cys Ser Ile Phe
167 305 310 315 320
168 Leu Trp Gly Gln Asn Thr Gly Phe Tyr Leu Leu Gly Asn Lys Pro Thr
169 325 330 335
170 Leu Asn Asn Leu Tyr Lys Pro Ser Thr Gln Asp Val Val Ala Ala Ser
171 340 345 350
172 Lys Lys Ser Ser Thr Trp Asp Tyr Trp Thr Ser Val Thr Pro Leu Ser
173 355 360 365
174 Gly Leu Cys Ile Trp Ser Thr Ile Phe Leu Val Ile Ser Gln Leu Val
175 370 375 380
176 Phe Gln Tyr His Pro Tyr Ser Val Ser Arg Arg Phe Ala Asn Leu Pro
177 385 390 395 400
178 Tyr Thr Leu Trp Val Ile Thr Tyr Asn Leu Leu Phe Leu Thr Gly Tyr
179 405 410 415
180 Cys Leu Thr Asp Lys Ile Phe Gly Asn Ser Ser Glu Tyr Tyr Lys Val
181 420 425 430
182 Ala Glu Cys Leu Glu Ser Ile Asn Ser Asn Gly Leu Phe Leu Phe Leu
183 435 440 445
184 Leu Ala Asn Val Ser Thr Gly Leu Val Asn Met Ser Met Val Thr Ile
185 450 455 460
186 Asp Ser Ser Pro Leu Lys Ser Phe Leu Val Leu Leu Ala Tyr Cys Ser
187 465 470 475 480
188 Phe Ile Ala Val Ile Ser Val Phe Leu Tyr Arg Lys Arg Ile Phe Ile
189 485 490 495
190 Lys Leu
192 <210> SEQ ID NO: 3
193 <211> LENGTH: 1458

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RAW SEQUENCE LISTING DATE: 08/08/2006
PATENT APPLICATION: US/10/536,935A TIME: 18:09:06

Input Set : N:\Crf4\Refhold\10_folder\J536935A.raw
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195 <213> ORGANISM: Candida albicans
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197 <221> NAME/KEY: CDS
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199 <400> SEQUENCE: 3
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202 1 5 10 15
203 act ggt ggc aca att gaa gaa att tat gct gta acc agt ata gca tta 96
204 Thr Gly Gly Thr Ile Glu Glu Ile Tyr Ala Val Thr Ser Ile Ala Leu
205 20 25 30
206 tca tct tat ttg tcc ttt aga ttg ttg aaa aag tct ctt ggt gat tta 144
207 Ser Ser Tyr Leu Ser Phe Arg Leu Leu Lys Ser Leu Gly Asp Leu
208 35 40 45
209 gct ttg att tac gac tac att ctt aat gtg ttg aca att cta gca tcc 192
210 Ala Leu Ile Tyr Asp Tyr Ile Leu Asn Val Leu Thr Ile Leu Ala Ser
211 50 55 60
212 att act gtt tat agc aac agc cct tct tat ttg cat tat tat ttg 240
213 Ile Thr Val Tyr Ser Asn Ser Pro Ser Tyr Leu His Tyr Phe Ile Val
214 65 70 75 80
215 att cca tca tta gtt ata tat cta gtg aat tac cat gtt gag aaa cca 288
216 Ile Pro Ser Leu Val Ile Tyr Leu Val Asn Tyr His Val Glu Lys Pro
217 85 90 95
218 tct tca ccc cat aga caa aat gat aca aaa gaa gat aaa tcg gac gaa 336
219 Ser Ser Pro His Arg Gln Asn Asp Thr Lys Glu Asp Lys Ser Asp Glu
220 100 105 110
221 cta ttg ccg aga aaa caa ttt ata aca gcc tat cgt tct caa atg ttg 384
222 Leu Leu Pro Arg Lys Gln Phe Ile Thr Ala Tyr Arg Ser Gln Met Leu
223 115 120 125
224 ata att act aat cta gct ata tta gct gtt gat ttt cct att ttc cca 432
225 Ile Ile Thr Asn Leu Ala Ile Leu Ala Val Asp Phe Pro Ile Phe Pro
226 130 135 140
227 aga aga ttt gcc aaa gtg gaa aca tgg ggc acg tca atg atg gat tta 480
228 Arg Arg Phe Ala Lys Val Glu Thr Trp Gly Thr Ser Met Met Asp Leu
229 145 150 155 160
230 gga gtt ggg tcg ttt gtg ttc tcc atg ggg ttg gct aat tct cga caa 528
231 Gly Val Gly Ser Phe Val Phe Ser Met Gly Leu Ala Asn Ser Arg Gln
232 165 170 175
233 ttg atc aag aac cac acc gac aac tac aaa ttt agt tgg aag agt tat 576
234 Leu Ile Lys Asn His Thr Asp Asn Tyr Lys Phe Ser Trp Lys Ser Tyr
235 180 185 190
236 ttg aaa aca atc aag cag aac ttt atc aag tca gtg cct ata ctt gtt 624
237 Leu Lys Thr Ile Lys Gln Asn Phe Ile Lys Ser Val Pro Ile Leu Val
238 195 200 205
239 tta gga gct att cgt ttt gtt agt gtt aag caa ttg gac tat cag gaa 672
240 Leu Gly Ala Ile Arg Phe Val Ser Val Lys Gln Leu Asp Tyr Gln Glu
241 210 215 220
242 cac gaa aca gag tat gga atc cat tgg aat ttt ttc ttc aca tta ggg 720
  
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VERIFICATION SUMMARY DATE: 08/08/2006
PATENT APPLICATION: US/10/536,935A TIME: 18:09:07

Input Set : N:\Crf4\Refhold\10_folder\J536935A.raw
Output Set: N:\CRF4\08082006\J536935A.raw

L:10 M:270 C: Current Application Number differs, Wrong Format
L:1009 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 12, CDS
LOCATION:44..2001
L:1012 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 12, CDS
LOCATION:44..2001
L:1057 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 12, CDS
LOCATION:44..2001
L:1060 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 12, CDS
LOCATION:44..2001
L:1102 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 12, CDS
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L:1105 M:351 W: Sequence data Name/Key Feature Out-of-Range, SEQ ID#: 12, CDS
LOCATION:44..2001